

A2



SEQUENCE LISTING

<110> BATHE, BRIGITTE

MOECKEL, BETTINA

PFEFFERLE, WALTER

HUTHMACHER, KLAUS

RUECKERT, CHRISTIAN

KALINOWSKI, JOERN

PUEHLER, ALFRED

BINDER, MICHAEL

GREISSINGER, DIETER

THIERBACH, GEORG

<120> NUCLEOTIDE SEQUENCES WHICH CODE FOR THE METE GENE

<130> 211710US0X

<140> 09/919,835

<141> 2001-08-02

<150> DE 10038023.9

<151> 2000-08-02

<150> DE 10109689.5

<151> 2001-02-28

<150> US 60/294,250

<151> 2001-05-31

<160> 8

<170> PatentIn version 3.1

<210> 1

<211> 2810

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (317)..(2551)

<223>

<400> 1

agcccaaaac ggcacatga atttaaattc ccggaacttc ttgacagacc gagcagtcta 60

gggttttggtt gaaaacgcaa tcggttcact tttaatcctc tccctggagc cccggatgat 120

gaggaacgcc aaagctttct gaatggaaat tttaagcgtt aagtgggacg acctcgatta 180

caaaaaggcg aggaaacccc cggggcagct ttctgccacc cggtgatttc gcgaaccttg 240

aaacatcgtc agaagattgc cgtgcgtcct agccgggatc cgcacgttcg gctcaagcag 300

aaagtcttta actcac atg act tcc aac ttt tct tcc act gtc gct ggt ctt 352

Met Thr Ser Asn Phe Ser Ser Thr Val Ala Gly Leu
1 5 10

cct cgc atc gga gcg aag cgt gaa ctg aag ttc gcg ctc gaa ggc tac 400

Pro Arg Ile Gly Ala Lys Arg Glu Leu Lys Phe Ala Leu Glu Gly Tyr
15 20 25

tgg aat gga tca att gaa ggt cgc gaa ctt gcg cag acc gcc cgc caa 448

Trp	Asn	Gly	Ser	Ile	Glu	Gly	Arg	Glu	Leu	Ala	Gln	Thr	Ala	Arg	Gln	
30						35					40					
ttg	gtc	aac	act	gca	tcg	gat	tct	ttg	tct	gga	ttg	gat	tcc	gtt	ccg	496
Leu	Val	Asn	Thr	Ala	Ser	Asp	Ser	Leu	Ser	Gly	Leu	Asp	Ser	Val	Pro	
45					50					55					60	
ttt	gca	gga	cgt	tcc	tac	tac	gac	gca	atg	ctc	gat	acc	gcc	gct	att	544
Phe	Ala	Gly	Arg	Ser	Tyr	Tyr	Asp	Ala	Met	Leu	Asp	Thr	Ala	Ala	Ile	
				65					70					75		
ttg	ggt	gtg	ctg	ccg	gag	cgt	ttt	gat	gac	atc	gct	gat	cat	gaa	aac	592
Leu	Gly	Val	Leu	Pro	Glu	Arg	Phe	Asp	Asp	Ile	Ala	Asp	His	Glu	Asn	
			80					85					90			
gat	ggt	ctc	cca	ctg	tgg	att	gac	cgc	tac	ttt	ggc	gct	gct	cgc	ggt	640
Asp	Gly	Leu	Pro	Leu	Trp	Ile	Asp	Arg	Tyr	Phe	Gly	Ala	Ala	Arg	Gly	
		95					100					105				
act	gag	acc	ctg	cct	gca	cag	gca	atg	acc	aag	tgg	ttt	gat	acc	aac	688
Thr	Glu	Thr	Leu	Pro	Ala	Gln	Ala	Met	Thr	Lys	Trp	Phe	Asp	Thr	Asn	
	110					115					120					
tac	cac	tac	ctc	gtg	ccg	gag	ttg	tct	gcg	gat	aca	cgt	ttc	gtt	ttg	736
Tyr	His	Tyr	Leu	Val	Pro	Glu	Leu	Ser	Ala	Asp	Thr	Arg	Phe	Val	Leu	
125					130					135					140	
gat	gcg	tcc	gcg	ctg	att	gag	gat	ctc	cgt	tgc	cag	cag	gtt	cgt	ggc	784
Asp	Ala	Ser	Ala	Leu	Ile	Glu	Asp	Leu	Arg	Cys	Gln	Gln	Val	Arg	Gly	
				145				150						155		
gtt	aat	gcc	cgc	cct	gtt	ctg	gtt	ggt	cca	ctg	act	ttc	ctt	tcc	ctt	832
Val	Asn	Ala	Arg	Pro	Val	Leu	Val	Gly	Pro	Leu	Thr	Phe	Leu	Ser	Leu	
			160					165					170			
gct	cgc	acc	act	gat	ggt	tcc	aat	cct	ttg	gat	cac	ctg	cct	gca	ctg	880
Ala	Arg	Thr	Thr	Asp	Gly	Ser	Asn	Pro	Leu	Asp	His	Leu	Pro	Ala	Leu	
		175					180					185				
ttt	gag	gtc	tac	gag	cgc	ctc	atc	aag	tct	ttc	gat	act	gag	tgg	gtt	928
Phe	Glu	Val	Tyr	Glu	Arg	Leu	Ile	Lys	Ser	Phe	Asp	Thr	Glu	Trp	Val	
	190					195					200					
cag	atc	gat	gag	cct	gcg	ttg	gtc	acc	gat	gtt	gct	cct	gag	gtt	ttg	976
Gln	Ile	Asp	Glu	Pro	Ala	Leu	Val	Thr	Asp	Val	Ala	Pro	Glu	Val	Leu	
205					210					215					220	
gag	cag	gtc	cgc	gct	ggt	tac	acc	act	ttg	gct	aag	cgc	gat	ggc	gtg	1024
Glu	Gln	Val	Arg	Ala	Gly	Tyr	Thr	Thr	Leu	Ala	Lys	Arg	Asp	Gly	Val	
				225					230					235		
ttt	gtc	aat	act	tac	ttc	ggc	tct	ggc	gat	cag	gcg	ctg	aac	act	ctt	1072

Phe	Val	Asn	Thr	Tyr	Phe	Gly	Ser	Gly	Asp	Gln	Ala	Leu	Asn	Thr	Leu	
			240					245					250			
gcg	ggc	atc	ggc	ctt	ggc	gcg	att	ggc	gtt	gac	ttg	gtc	acc	cat	ggc	1120
Ala	Gly	Ile	Gly	Leu	Gly	Ala	Ile	Gly	Val	Asp	Leu	Val	Thr	His	Gly	
		255					260					265				
gtc	act	gag	ctt	gct	gcg	tgg	aag	ggc	gag	gag	ctg	ctg	gtt	gcg	ggc	1168
Val	Thr	Glu	Leu	Ala	Ala	Trp	Lys	Gly	Glu	Glu	Leu	Leu	Val	Ala	Gly	
	270					275						280				
atc	gtt	gat	ggc	cgt	aac	att	tgg	cgc	acc	gac	ctg	tgt	gct	gct	ctt	1216
Ile	Val	Asp	Gly	Arg	Asn	Ile	Trp	Arg	Thr	Asp	Leu	Cys	Ala	Ala	Leu	
285					290					295					300	
gct	tcc	ctg	aag	cgc	ctg	gca	gct	cgc	ggc	cca	atc	gca	gtg	tct	acc	1264
Ala	Ser	Leu	Lys	Arg	Leu	Ala	Ala	Arg	Gly	Pro	Ile	Ala	Val	Ser	Thr	
				305					310					315		
tct	tgt	tca	ctg	ctg	cac	gtt	cct	tac	acc	ctc	gag	gct	gag	aac	att	1312
Ser	Cys	Ser	Leu	Leu	His	Val	Pro	Tyr	Thr	Leu	Glu	Ala	Glu	Asn	Ile	
			320					325					330			
gag	cct	gag	gtc	cgc	gac	tgg	ctt	gcc	ttc	ggc	tcg	gag	aag	atc	acc	1360
Glu	Pro	Glu	Val	Arg	Asp	Trp	Leu	Ala	Phe	Gly	Ser	Glu	Lys	Ile	Thr	
		335					340					345				
gag	gtc	aag	ctg	ctt	gcc	gac	gcc	cta	gcc	ggc	aac	atc	gac	gcg	gct	1408
Glu	Val	Lys	Leu	Leu	Ala	Asp	Ala	Leu	Ala	Gly	Asn	Ile	Asp	Ala	Ala	
	350					355					360					
gcg	ttc	gat	gcg	gcg	tcc	gca	gca	att	gct	tct	cga	cgc	acc	tcc	cca	1456
Ala	Phe	Asp	Ala	Ala	Ser	Ala	Ala	Ile	Ala	Ser	Arg	Arg	Thr	Ser	Pro	
365					370					375					380	
cgc	acc	gca	cca	atc	acg	cag	gaa	ctc	cct	ggc	cgt	agc	cgt	gga	tcc	1504
Arg	Thr	Ala	Pro	Ile	Thr	Gln	Glu	Leu	Pro	Gly	Arg	Ser	Arg	Gly	Ser	
				385					390					395		
ttc	gac	act	cgt	gtt	acg	ctg	cag	gag	aag	tca	ctg	gag	ctt	cca	gct	1552
Phe	Asp	Thr	Arg	Val	Thr	Leu	Gln	Glu	Lys	Ser	Leu	Glu	Leu	Pro	Ala	
			400					405					410			
ctg	cca	acc	acc	acc	att	ggc	tct	ttc	cca	cag	acc	cca	tcc	att	cgt	1600
Leu	Pro	Thr	Thr	Thr	Ile	Gly	Ser	Phe	Pro	Gln	Thr	Pro	Ser	Ile	Arg	
		415					420					425				
tct	gct	cgc	gct	cgt	ctg	cgc	aag	gaa	tcc	atc	act	ttg	gag	cag	tac	1648
Ser	Ala	Arg	Ala	Arg	Leu	Arg	Lys	Glu	Ser	Ile	Thr	Leu	Glu	Gln	Tyr	
	430					435					440					
gaa	gag	gca	atg	cgc	gaa	gaa	atc	gat	ctg	gtc	atc	gcc	aag	cag	gaa	1696

Glu 445	Glu	Ala	Met	Arg	Glu 450	Glu	Ile	Asp	Leu	Val 455	Ile	Ala	Lys	Gln	Glu 460	
gaa	ctt	ggt	ctt	gat	gtg	ttg	gtt	cac	ggt	gag	cca	gag	cgc	aac	gac	1744
Glu	Leu	Gly	Leu	Asp 465	Val	Leu	Val	His	Gly 470	Glu	Pro	Glu	Arg	Asn 475	Asp	
atg	gtt	cag	tac	ttc	tct	gaa	ctt	ctc	gac	ggt	ttc	ctc	tca	acc	gcc	1792
Met	Val	Gln	Tyr 460	Phe	Ser	Glu	Leu	Leu 465	Asp	Gly	Phe	Leu	Ser 490	Thr	Ala	
aac	ggc	tgg	gtc	caa	agc	tac	ggc	tcc	cgc	tgt	gtt	cgt	cct	cca	gtg	1840
Asn	Gly	Trp 495	Val	Gln	Ser	Tyr	Gly 500	Ser	Arg	Cys	Val	Arg 505	Pro	Pro	Val	
ttg	ttc	gga	aac	gtt	tcc	cgc	cca	gcg	cca	atg	act	gtc	aag	tgg	ttc	1888
Leu	Phe 510	Gly	Asn	Val	Ser	Arg 515	Pro	Ala	Pro	Met	Thr 520	Val	Lys	Trp	Phe	
cag	tac	gca	cag	agc	ctg	acc	cag	aag	cat	gtc	aag	gga	atg	ctc	acc	1936
Gln	Tyr	Ala	Gln	Ser	Leu	Thr 530	Gln	Lys	His	Val 535	Lys	Gly	Met	Leu	Thr 540	
ggt	cca	gtc	acc	atc	ctt	gca	tgg	tcc	ttc	gtt	cgc	gat	gat	cag	ccg	1984
Gly	Pro	Val	Thr	Ile 545	Leu	Ala	Trp	Ser	Phe 550	Val	Arg	Asp	Asp	Gln 555	Pro	
ctg	gct	acc	act	gct	gac	cag	gtt	gca	ctg	gca	ctg	cgc	gat	gaa	att	2032
Leu	Ala	Thr	Thr 560	Ala	Asp	Gln	Val	Ala 565	Leu	Ala	Leu	Arg	Asp 570	Glu	Ile	
aac	gat	ctc	atc	gag	gct	ggc	gcg	aag	atc	atc	cag	gtg	gat	gag	cct	2080
Asn	Asp	Leu 575	Ile	Glu	Ala	Gly 580	Ala	Lys	Ile	Ile	Gln	Val 585	Asp	Glu	Pro	
gcg	att	cgt	gaa	ctg	ttg	ccg	cta	cga	gac	gtc	gat	aag	cct	gcc	tac	2128
Ala	Ile 590	Arg	Glu	Leu	Leu	Pro 595	Leu	Arg	Asp	Val	Asp 600	Lys	Pro	Ala	Tyr	
ctg	cag	tgg	tcc	gtg	gac	tcc	ttc	cgc	ctg	gcg	act	gcc	ggc	gca	ccc	2176
Leu	Gln	Trp	Ser	Val	Asp 610	Ser	Phe	Arg	Leu	Ala 615	Thr	Ala	Gly	Ala	Pro 620	
gac	gac	gtc	caa	atc	cac	acc	cac	atg	tgc	tac	tcc	gag	ttc	aac	gaa	2224
Asp	Asp	Val	Gln 625	Ile	His	Thr	His	Met	Cys 630	Tyr	Ser	Glu	Phe	Asn 635	Glu	
gtg	atc	tcc	tcg	gtc	atc	gcg	ttg	gat	gcc	gat	gtc	acc	acc	atc	gaa	2272
Val	Ile	Ser	Ser 640	Val	Ile	Ala	Leu	Asp 645	Ala	Asp	Val	Thr	Thr 650	Ile	Glu	
gca	gca	cgt	tcc	gac	atg	cag	gtc	ctc	gct	gct	ctg	aaa	tct	tcc	ggc	2320

Ala	Ala	Arg	Ser	Asp	Met	Gln	Val	Leu	Ala	Ala	Leu	Lys	Ser	Ser	Gly	
	655						660					665				
ttc	gag	ctc	ggc	gtc	gga	cct	ggg	gtg	tgg	gat	atc	cac	tcc	ccg	cgc	2368
Phe	Glu	Leu	Gly	Val	Gly	Pro	Gly	Val	Trp	Asp	Ile	His	Ser	Pro	Arg	
	670						675				680					
ggt	cct	tcc	gcg	cag	gaa	gtg	gac	ggg	ctc	ctc	gag	gct	gca	ctg	cag	2416
Val	Pro	Ser	Ala	Gln	Glu	Val	Asp	Gly	Leu	Leu	Glu	Ala	Ala	Leu	Gln	
	685					690					695				700	
tcc	gtg	gat	cct	cgc	cag	ctg	tgg	gtc	aac	cca	gac	tgt	ggg	ctg	aag	2464
Ser	Val	Asp	Pro	Arg	Gln	Leu	Trp	Val	Asn	Pro	Asp	Cys	Gly	Leu	Lys	
				705					710					715		
acc	cgt	gga	tgg	cca	gaa	gtg	gaa	gct	tcc	cta	aag	gtt	ctc	gtt	gag	2512
Thr	Arg	Gly	Trp	Pro	Glu	Val	Glu	Ala	Ser	Leu	Lys	Val	Leu	Val	Glu	
			720					725					730			
tcc	gct	aag	cag	gct	cgt	gag	aaa	atc	gga	gca	act	atc	taaattgggt			2561
Ser	Ala	Lys	Gln	Ala	Arg	Glu	Lys	Ile	Gly	Ala	Thr	Ile				
		735					740					745				
taccgctagg	aacccaaaga	ttaagggcac	gagtgtcacc	aggattgccg	cacccatggc											2621
aacaccgaag	gacaccgtgc	ccactcctat	ttgcatcaca	gcgcccaagg	tagcggcgcc											2681
caaaacagcg	cccacctggc	gtgaggtgtt	gtaaaaacca	gaagcagagc	ccactaaatc											2741
ctgcggaaca	tcacgcagag	caatcacaga	gttcggtgca	aaactcatcg	cgttggagct											2801
accgaacaa																2810

<210> 2

<211> 745

<212> PRT

<213> Corynebacterium glutamicum

<400> 2

Met	Thr	Ser	Asn	Phe	Ser	Ser	Thr	Val	Ala	Gly	Leu	Pro	Arg	Ile	Gly
1				5					10					15	

Ala	Lys	Arg	Glu	Leu	Lys	Phe	Ala	Leu	Glu	Gly	Tyr	Trp	Asn	Gly	Ser
			20					25					30		

Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr
35 40 45

Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg
50 55 60

Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu
65 70 75 80

Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro
85 90 95

Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu
100 105 110

Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu
115 120 125

Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala
130 135 140

Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg
145 150 155 160

Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr
165 170 175

Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr
180 185 190

Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu
195 200 205

Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg
210 215 220

Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr
225 230 235 240

Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly
245 250 255

Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu
260 265 270

Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly
275 280 285

Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys
290 295 300

Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu
305 310 315 320

Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val
325 330 335

Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu
340 345 350

Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala
355 360 365

Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro
370 375 380

Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg
385 390 395 400

Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr
405 410 415

Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala
420 425 430

Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met
435 440 445

Arg Glu Glu Ile Asp Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu
450 455 460

Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr
465 470 475 480

Phe Ser Glu Leu Leu Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val
485 490 495

Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn
500 505 510

Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln
515 520 525

Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr
530 535 540

Ile Leu Ala Trp Ser Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr
545 550 555 560

Ala Asp Gln Val Ala Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile
565 570 575

Glu Ala Gly Ala Lys Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu
580 585 590

Leu Leu Pro Leu Arg Asp Val Asp Lys Pro Ala Tyr Leu Gln Trp Ser
595 600 605

Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp Val Gln
610 615 620

Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu Val Ile Ser Ser
625 630 635 640

Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu Ala Ala Arg Ser
645 650 655

Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly Phe Glu Leu Gly
660 665 670

Val Gly Pro Gly Val Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala
675 680 685

Gln Glu Val Asp Gly Leu Leu Glu Ala Ala Leu Gln Ser Val Asp Pro
690 695 700

Arg Gln Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Trp
705 710 715 720

Pro Glu Val Glu Ala Ser Leu Lys Val Leu Val Glu Ser Ala Lys Gln
725 730 735

Ala Arg Glu Lys Ile Gly Ala Thr Ile
740 745

<210> 3

<211> 41

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic DNA

<400> 3

agaacgaatt caaaggagga caaccatgcc caccctcgcg c

41

<210> 4

<211> 31

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic DNA

<400> 4

gtcgtggatc ccctattaga tgtagaactc g

31

<210> 5

<211> 47

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic DNA

<400> 5

ggctcaaaga tctaaaggag gacaaccatg acttccaact tttcttc

47

<210> 6

<211> 40

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic DNA

<400> 6

ggttcctgtc gacggtacca tttagatagt tgctccgatt

40

<210> 7

<211> 42

<212> DNA

<213> Artificial sequence

A2
cont.
<220>

<223> Synthetic DNA

<400> 7

ctaataagtc gacaaaggag gacaaccatg ccaaagtacg ac

42

<210> 8

<211> 33

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic DNA

<400> 8

gagtctaagc catgctagat tgcagcaaag ccg

33